

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 4, 2002, 01:26:26 ; Search time 13.806 seconds/
(without alignments)
1105.559 Million cell updates/sec

Title: US-09-805-550-4

Perfect score: 1910

Sequence: 1 MKLTVKLTGKTHFEIRVOPN.....CDRDELALNYLLHAGEED 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	634	33.2	416	1	R23B_MOUSE
2	625.5	32.7	409	1	R23B_HUMAN
3	603.5	31.6	363	1	R23A_HUMAN
4	597.5	31.3	363	1	R23A_MOUSE
5	561.5	29.4	368	1	RH23_SCHPO
6	403	21.1	398	1	RA23_YEAST
7	163.5	8.6	354	1	YANG_SCHPO
8	154	8.1	373	1	DSK2_YEAST
9	122.5	6.4	76	1	UBI0_DROME
10	122.5	6.4	76	1	UBI0_HUMAN
11	122	6.4	979	1	REF1_HUMAN
12	121.5	6.4	81	1	NEB8_HUMAN
13	121.5	6.4	81	1	NEB8_MOUSE
14	120.5	6.3	76	1	UBI0_EIMBO
15	118.5	6.2	76	1	UBI0_LEIMA
16	118.5	6.2	76	1	UBI0_PHYIN
17	118.5	6.2	76	1	UBI0_STRPU
18	117.5	6.2	76	1	UBI0_LEITA
19	116.5	6.1	76	1	UBI0_ACACA
20	116.5	6.1	76	1	UBI0_NEUCR
21	115.5	6.0	93	1	UBI1_NEVOP
22	114.5	6.0	76	1	UBI0_AGLNE
23	114.5	6.0	76	1	UBI0_CAEEL
24	114.5	6.0	76	1	UBI0_YEAST
25	113.5	5.9	76	1	UBI0_ACECL
26	113.5	5.9	76	1	UBI0_CHIRE
27	113.5	5.9	76	1	UBI0_COPCO
28	113.5	5.9	76	1	UBI0_TRYCR
29	113	5.9	392	1	HME1_HUMAN
30	113	5.9	989	1	FRO_NEUCR
31	112.5	5.9	76	1	UBI0_SOYBN
32	112.5	5.9	76	1	UBI0_TETPY
33	111	5.8	1132	1	BAT3_HUMAN

34	111	5.8	1144	1	RIR1_HSV23	P09853 herpes simp
35	110.5	5.8	76	1	UBI0_EUPBL	P23324 euploles eu
36	109.5	5.7	76	1	UBI0_TRYBB	P15174 trypanosoma
37	108.5	5.7	76	1	UBI0_DICDI	P08618 dictyostell
38	108	5.7	910	1	PERT_BORPE	P14283 bordetella
39	108	5.7	1102	1	RPOB_SYNY3	P77965 synechocyst
40	107.5	5.6	1618	1	NEST_HUMAN	P48681 homo sapien
41	107	5.6	567	1	ODP2_HAEIN	P45118 haemophilus
42	106.5	5.6	701	1	CGI_HUMAN	Q13495 homo sapien
43	106.5	5.6	975	1	CUT1_CANPA	P39881 canis fam11
44	106	5.5	1036	1	NIT2_NEUCR	P19212 neurospora
45	106	5.5	1113	1	MYSD_DICDI	P34109 dictyostell

ALIGNMENTS

RESULT 1
R23B_MOUSE
ID R23B_MOUSE STANDARD; PRT; 416 AA.
AC P54728;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE UV excision repair protein Rad23 homolog B (HNR23B) (XP-C repair
DE complementing complex 58 kDa protein) (P58).
GN RAD23B OR HNR23B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Testis;
RX MEDLINE=96403997; PubMed=8808275;
RA van der Spek P.J., Visser C.E., Hanaoka F., Smit B.,
RA Hagemeijer A., Bootsma D., Hoeljmakers J.H.J.;
RT Cloning, comparative mapping, and RNA expression of the mouse
RT homologues of the Saccharomyces cerevisiae nucleotide excision repair
RT gene RAD23.*;
RL Genomics 31:20-27(1996).
CC - FUNCTION: INVOLVED IN DNA EXCISION REPAIR. MAY PLAY A PART IN DNA
CC DAMAGE RECOGNITION AND/OR IN ALTERING CHROMATIN STRUCTURE TO
CC ALLOW ACCESS BY DAMAGE-PROCESSING ENZYMES.
CC - SUBUNIT: HETERODIMER OF A 125 kDa SUBUNIT (P125) AND OF A
CC 58 kDa SUBUNIT (P58).
CC - SUBCELLULAR LOCATION: Nuclear (Probable).
CC - SIMILARITY: CONTAINS 2 UBA DOMAINS.
CC - SIMILARITY: CONTAINS 2 UBA DOMAINS.
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CC or send an email to license@sib-sib.ch).
DR EMBL: X97411; CA63146.1; -
DR HSSP: P54725; IDV0.
DR MGD: MGI:105128; Rad23b.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00240; ubiquitin; 1.
DR Pfam: PF00627; UBA; 2.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBA; 1.
DR TIGRFAMs: TIGR00601; rad23; 1.
DR PROSITE: PS50053; UBIQUITIN_2; 1.
KW DNA damage; DNA repair; Nuclear protein.
FT DOMAIN 1 79 UBIQUITIN-LIKE.
FT DOMAIN 255 261 POLY-ALA.

FT	DOMAIN	262	270	POLY-THR.
FT	DOMAIN	336	355	POLY-GLY.
SEQ	SEQUENCE	416 AA:	43516 MM:	13E0245ABD892205 CRC64:
	Query Match	33.2%:	Score 634:	DB 1; Length 416:
	Best Local Similarity	33.5%:	Pred. No. 1.4e-33:	
	Matches 146:	Conservative 93:	Mismatches 109:	Indels 88; Gaps 11:
OY	1 MKLYTKLKGHFELRVQNDYIMAVKKNIEIIOGRKDSIPMGQOLLIFNGKLYKDESTIE	60		
DB	1 MOVYTKLQOQTEFKDIDDEETVYKALKEIESEKGNDAFVAGOKLYAGKILSDTAK	60		
OY	61 ENKVNDEDFVLVMSLKGKTSGSTSSOSHNTPA---TRQAPPEAPQ-QAPPPVAPI	116		
DB	61 EKKIDKKNFYVYMKPRAYTAVATITQPSSTPPTVSSPVAQAAPPTALAPT	120		
OY	117 TT-----SOPE---GLPQAP-----NTHDNA	135		
DB	121 STPTASTPASTVASEPAPAGATQEKPRKAQIPIVLTSPAPADSTPQDSSRSNLFEDA	180		
OY	136 ASNLISGRNVDTIINQLEMGGSGDKDQVQALPRAIYNPRAVELYSGIPVATETIV	195		
DB	181 TSAVLTGGSYEMVAVTEIMSG---YERQVYIATLASFNNPDAVEYLYLGMGIPGRESQA	237		
OY	196 PLGGGAMTTRDAPRGEGLSGIPMTAPLDLPGQASNAG-----GGAGGCPIDFLRN	248		
DB	238 VVD-----PPQAVSTGPS-----PVAALAAATTTATTTTSGGHPLEFLRN	281		
OY	249 NFOQVAREMVTNPOIILQPMLETSKONPOILRLIEHNDEFLQILNPEP-----	300		
DB	282 QPQFQMMQIIOGNSSLPLALQIGRENPQLOQISQHEHFIQMLNPNVQEGAGGGGG	341		
OY	301 -----GGSEDFLDQPEDEMPAIVTPEQDAIGRLSEMGCDRAIVATFLACDRN	352		
DB	342 GGGGGGGGGGGGGGAEAGSGHMNY-IQVTPQEKATIERLKALGPEPGLVQAYFACERK	400		
OY	353 EELANVYLHAGEED 368			
DB	401 EELANVFLQONFDED 416			
RESULT 2				
R23B_HUMAN	R23B_HUMAN	STANDARD:	PRT:	409 AA.
AC	P54727			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	UV excision repair protein RAD23 homolog B (HHR23B) (XP-C repair			
DE	complementing complex 58 kDa protein) (P58).			
GN	RAD23B.			
OS	Human sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
NCBI_Taxid	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE-94222030; PubMed-8168482;			
RA	Masutani C., Sugawara K., Yanagisawa J., Sonoyama T., Ui M.,			
RA	Emomoto T., Takio K., Tanaka K., van der Spek P.J., Bootsma D.,			
RA	Hoeltmakers J.H.J., Hanaoka F.;			
RT	"Purification and cloning of a nucleotide excision repair complex			
RT	involving the xeroderma pigmentosum group C protein and a human			
RT	homologue of yeast RAD23.";			
RL	EMBO J. 13:1831-1843(1994).			
CC	-1- FUNCTION: INVOLVED IN DNA EXCISION REPAIR. MAY PLAY A PART IN DNA			
CC	DAMAGE RECOGNITION AND/OR IN ALTERING CHROMATIN STRUCTURE TO			
CC	ALLOW ACCESS BY DAMAGE-PROCESSING ENZYMES.			
CC	-1- SUBUNIT: Heterodimer of a 125 kDa subunit (p125) and of a			
CC	58 kDa subunit (p58). Interacts with MTD.			
CC	-1- SUBCELLULAR LOCATION: Nuclear (Probable).			
CC	-1- DOMAIN: The ubiquitin-like domain mediates interaction with MTD.			
CC	-1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.			

	-	SIMILARITY: CONTAINS 2 UBA DOMAINS.	
CC	-----		
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration	
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CC	-----		
DR		EMBL; D21090; BAA04652.1; .	
DR	HSSP; P54725; IDV0.		
DR	GeneW; HGNC:9813; RAD23B.		
DR	MIM: 600062; .		
DR	InterPro; IPR004806; Rad23.		
DR	InterPro; IPR000449; UBA_domain.		
DR	InterPro; IPR000626; Ubiquitin.		
DR	Pfam; PF00247; ubiqutin; 1.		
DR	Pfam; PF00627; UBA; 2.		
DR	SMART; SM00165; UBA; 2.		
DR	SMART; SM00213; UBO; 1.		
DR	TIGRFAMs; TIGR00601; rad23; 1.		
DR	ProSITE; PS50053; UBQUITIN_2; 1.		
KW	DNA damage; DNA repair; Nuclear protein.		
FT	DOMAIN 1 79	UBQUITIN-LIKE.	
FT	DOMAIN 103 106	POLY-THR.	
FT	DOMAIN 254 260	POLY-ALA.	
FT	DOMAIN 261 269	POLY-THR.	
FT	DOMAIN 336 348	POLY-GLY.	
SQ	SEQUENCE 409 AA; 43171 MW; C026C78273BCB289 CNC64;		
Query Match	32.7%; Score 625.5; DB 1; Length 409;		
Matches 147; Conservative	34.8%; Pred. No. 4.6e-33;		
	Match 83; Indels 67; Gaps 11;		
OY	1 MKLVTKLTGTFEFLRYOQNDITMAVKKNIIELOGSDSYPMWGOLLIFNGKYLKDSESTLE 60		
DB	1 MGVTKTLQQOCTFKKIDIDEETVKKALKEIKESKGDAFPVAGQKLITAGKITLINDDTALK 60		
OY	61 ENKNVEDGFLVVLMSRKGT-----SGSTGTSQSHTSPATROAP---PLEAFO 106		
DB	61 EKXIDENKNNVVVMYWKPKAVSTRPARATTQGSAPASTYATVSTTTTYVAQAIPVPALAPT 120		
OY	107 QAP-----QP-PVAPIITTSQPEGLPAQAP-----NTHDNA 135		
DB	121 STTPASITPASATASSEPPASPASAOKEPAPKEPATRPVATSPATDSTGSSRSNLFEDE 180		
OY	136 ASNLISGRNVDTIINQMELMGSGSKDKOVQALRAAYNNPRAVEYLYLSGIPTVAET-A 194		
DB	181 TSAVTGGOSYEKMVVEIISMVG--YEREQVIALLRSEFNNPRAVEYLYLMGITPGRESQA 237		
OY	195 VPIGGOGANTTEPRATTEGEAGISGIPNTAVLDLPQGASNAGGAGGAPLDPLRNPNPOFA 254		
DB	238 VYDPQQAOST--GAQOSSVAALAAATTT-----ATTTTSSSGHPLEFLIRNPQPOQ 287		
OY	235 VAEVYTNPDQIIQPMVLVELSKONPOLRLRIENHDEFQLLNPEP-----GEGGFIDL 308		
DB	288 MQQIQNPSPILPALLOIGRENPDQLQISOHQEHFIOMNEPYOEAGQGCGGGGGSG 347		
OY	309 QPEEDMEPHA--ISTVPEQEAIIGRLSEGPFPRARYTEFLACDNREELAAVYLEHAGE 366		
DB	348 GIAEGSGHMNYIOVTPQEKAEIERLKALGPEDEGLVIAVFACENKENMLANFLAQOND 407		
OY	367 ED 368		
DB	408 ED 409		
RESULT 3			
R23A_HUMAN			
ID R23A_HUMAN	STANDARD; PRt:	363 AA.	
AC P54725;			
DT 01-OCT-1996 (Rel. 34, Created)			

01-OCT-1996 (Rel. 34, last sequence update)
15-JUN-2002 (Rel. 41, last annotation update)
UV excision repair protein RAD23 homolog A (HHR23A).
RAD23A.
Homo sapiens (human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=94222030; PubMed=8168482;
RA Mesutani C., Sugawara K., Yanagisawa J., Sonoyama T., Uj M.,
RA Enomoto T., Takio K., Tanaka K., van der Spek P.O., Bootsma D.,
RA Hoeljmakers J.H.J., Hanaoka F.;
RT Purification and cloning of a nucleotide excision repair complex
involving the xeroderma pigmentosum group C protein and a human
RT homologue of yeast Rad23.";
RL EMBO J. 13:1831-1843(1994).
[2]
SEQUENCE FROM N.A.
RA Lamerdin J., McCreedy P., Stillwagen S., Ramirez M., Carrano A.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
[3]
RP STRUCTURE BY NMR OF 319-363.
RX MEDLINE=99061330; PubMed=9846873;
RA Dieckmann T., Withers-Ward E.S., Jarosinski M.A., Liu C.F.,
RA Chen I.S.Y., Felgou J.;
RT "Structure of a human DNA repair protein UBA domain that interacts
RT with HIV-1 Vpr.";
RL Nat. Struct. Biol. 5:1042-1047(1998).
[4]
RP STRUCTURE BY NMR OF 319-363.
RX MEDLINE=20541363; PubMed=11087358;
RA Withers-Ward E.S., Mueller T.D., Chen I.S.Y., Felgou J.;
RT "Biochemical and structural analysis of the interaction between the
RT UBA(2) domain of the DNA repair protein HHR23A and HIV-1 Vpr.";
RL Biochemistry 39:14103-14112(2000).
CC -1- FUNCTION: Involved in postreplication repair of UV-damaged DNA.
CC Postreplication repair functions in gap-filling of a daughter
CC strand on replication of damaged DNA (Potential).
CC -1- SUBUNIT: Interacts with MJD.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- DOMAIN: The ubiquitin-like domain mediates interaction with MJD.
CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 UBA DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D12335; BAA04767.1; -;
DR EMBL: AD000092; AAB51177.1; -;
DR PDB: 1DVO; 11-FEB-00.
DR Genew; HGNC:9812; RAD23A.
DR MIM: 600061; -;
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00240; ubiquitin; 1.
DR Pfam: PF00627; UBA; 2.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBO; 1.
DR TIGRfam: TIGR00601; rad23; 1.
DR PROSITE: PS50053; UBIQUITIN_2; 1.
KW DNA damage; DNA repair; Nuclear protein; 3D-structure.
FT DOMAIN 1 81 UBIQUITIN-LIKE.
SQ SEQUENCE 363 AA; 39609 MW; C4E47E9313B47B5 CRC64;
Query Match 31.6%; Score 603.5; DB 1; Length 363;

Best Local Similarity 33.4%; Pred. No. 1e-31;
Matches 133; Conservative 88; Mismatches 106; Indels 71; Gaps 8;
OY 3 LTVKLTGTHFEIRYQPDITIAVAKNIEEIOGKSYPMWGOGLIFNGKIDESTLEEN 62
D 5 ITLKLQOQTRKIRNEPEETVYKLEKEIAEKGRAFPVAAOKLIYAKLISDDPINDY 64
OY 63 KVNEDGLVWMLSKGKTSSTGSSOHSNTPARQAPPLBAPOQAPVPVAPIT- 117
D 65 RIDENKFFVAVVT--KTRAGOGTS-----APPEASPTAPPESTSFPPAPSGMSH 114
OY 118 -----TSQPECLPAQAPNT-----HDNAASNLISGRVNDITINQIMMG 156
D 115 PPAAREDKSPSEESAPPTSPESVSGVSSSGREEDASTLVYGSSEYETMLTEIMSG 174
OY 157 GGSMDKDVORALRAYNNPERAVEYLSGIPVTAIEAIVPGOGANTDAPAGEALTS 216
D 175 ---YERERVAALRASTNNPRAVEYLTGTP-----GSPPEGSGVQESQVS 219
OY 217 GIPNTAPLDLPPGASNAGGAGGGLDPLFRNNPQFQVAREMVTNPQILQPMLELSKQ 276
D 220 EQPATE-----AAGENPTEFLRDQPFQMRQVIOQNPAIPLALLQQLQGE 265
OY 277 NPQILRIEENHDEFLQLNEP-----FEGEGDFLDQPEDEMPHAISTVPEQEAIG 330
D 266 NPQLQOQISRHQEQFIQMLNEPPEGLADISDEGEVGAIGEAQPMNYIQVTPOKEAIE 325
OY 331 RLESMPDRAVIEFAFLACDRNEELAAANYLLEHAGEED 368
D 326 RLKALGPPESLVIOAYFACENKNEIANPILLSQNFDE 363
RESULT 4
R23A_MOUSE
ID R23A_MOUSE STANDARD; PRT: 363 AA.
AC P54726;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE UV excision repair protein RAD23 homolog A (HHR23A).
GN RAD23A OR HHR23A.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
CC [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-Testis;
RX MEDLINE=96403997; PubMed=8808275;
RA van der Spek P.J., Visser C.E., Hanaoka F., Smit B.,
RA Hagemeijer A., Bootsma D., Hoeljmakers J.H.J.;
RT "Cloning, comparative mapping, and RNA expression of the mouse
RT homologues of the Saccharomyces cerevisiae nucleotide excision repair
RT gene RAD23.";
RL Genomics 31:20-27(1996).
CC -1- FUNCTION: Involved in postreplication repair of UV-damaged DNA.
CC Postreplication repair functions in gap-filling of a daughter
CC strand on replication of damaged DNA (Potential).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 UBA DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X92410; CAA63145.1; -;
DR HSSP: P54725; 1DVO.
DR MGD; MGI:105126; Rad23a.

```
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; Uba_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00240; ubiquitin; 1.
DR Pfam: PF00627; UBA; 2.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBO; 2.
DR TIGRFAMs: TIGR00601; Rad23; 1.
DR PROSITE: PS50053; Ubiquitin-2; 1.
KW DNA damage; DNA repair; Nuclear protein.
FT DOMAIN 1
SQ SEQUENCE 363 AA; 39769 MW; 67EAB96EEBA5C203 CRC64;

Query Match 31.3%; Score 597.5; DB 1; Length 363;
Best Local Similarity 33.7%; Pred. No. 2,4e-31;
Matches 136; Conservative 84; Mismatches 101; Indels 83; Gaps 11;

OY 3 LNVKTLKGFHEIRVQPNDTIMAVKKNIEIQQKDSYPMGQQLIFNGVKLDESTLEEM 62
DB 5 TLTKTQQQTFKIRMPDETIVKYLKEIKERKQKAPVAGQKLITAGKILSDVPTRDY 64
OY 63 KVNEDGLVYMLSKGTSGSTGTSSQSHNTPATRQAPLEAPQAPQ--PVAPI---- 116
DB 65 HIDEKFNVVVYTKAK--AGGGIS-----APPEASPTAVPEPSTPEPPVLASG 110
OY 117 -----TTSQPEGLPAQAPNT-----HDNAASMLSGRNVDTIINQL 152
DB 111 MSHPPPTSEDSKSPSEESTTTSPEISGSVPSSSGSGREEDASALVMSGEYEMLTET 170
OY 153 MEMGSGMDKDKYQALRAAYNPERAVELYSGIPVTAELIAPVIGGQANTDRA--PT 210
DB 171 MSGG---YERENVVALRASYNPHAVEXLTLGTGSP---PEIG-SVQEQRAEQRA 223
OY 211 GEAGLSGIPNTAPLDLFPQAGSNAGGAGCGPLDLRNPPQPAVREMYVNTNQLQPMI 270
DB 224 TEA-----ACENPLEFLRDPQFOQNMQRQVQIQQNPAFLPALL 259
OY 271 VELSKQNPQILRIENHDEFLQINEP-----FEGGSGDLFDQEEDEMPAIAIVTPE 324
DB 260 QQLGGQNPQLQDISHQOFQIOMLNEPPEGLADISDVGEVGAIGEAAPQMYIQTVPQ 319
OY 325 EDEAIGRLSEMGFRRARVIEAFLACDRNEELANLYLLEHAGEED 368
DB 320 EKEAIEIRLAKLGPESLVIQAVFACKENMLANFLLSQNFDE 363

RESULT 5
RH23_SCHPO
ID RH23_SCHPO STANDARD; PRT: 368 AA.
AC 074803:
DR 15-JUN-2002 (Rel. 41, Created)
DR 15-JUN-2002 (Rel. 41, Last sequence update)
DR 15-JUN-2002 (Rel. 41, Last annotation update)
DE UV excision repair protein rhp23 (RAD23 homolog).
GN RHP23 OR SPBC2D10.12.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
RC STRAIN=SP223;
RA Pubmed-11788722;
RA Elder R.T., Song X.-Q., Chen M., Hopkins K.M., Lieberman H.B.,
RA Zhao Y.;
RA "Involvement of rhp23, a Schizosaccharomyces pombe homolog of the
RT human HHR23A and Saccharomyces cerevisiae RAD23 nucleotide excision
RT repair genes, in cell cycle control and protein ubiquitination.";
RL Nucleic Acids Res. 30:561-591(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
```

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RX MEDLINE-21848401; PubMed-11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hildalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsis K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoult B.,
RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Meestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnardt H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wandut R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
RN [3]
RP CHARACTERIZATION.
RX PubMed-10652327;
RA Lombaerts M., Goeloe J.L., den Dulk H., Brandsma J.A., Brouwer J.;
RT "Identification and characterization of the rhp23(+) DNA repair gene
RT in Schizosaccharomyces pombe.";
RL Biochem. Biophys. Res. Commun. 268:210-215(2000).
CC -!- FUNCTION: Involved in postreplication repair of UV-damaged DNA.
CC Postreplication repair functions in gap-filling of a daughter
CC strand on replication of damaged DNA.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: CONTAINS 1 UBIOURIN-LIKE DOMAIN.
CC
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CC or send an email to license@sib-sib.ch).
CC
DR EMBL: AF174293; AAD51975.1; -.
DR EMBL: AL031788; CAA21170.1; -.
DR HSSP: P54725; IDVO.
DR InterPro: IPR000449; UBA.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiquitin; 1.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBO; 2.
DR PROSITE: PS50053; Ubiquitin-2; 1.
KW DNA damage; DNA repair; Nuclear protein.
FT DOMAIN 1
FT DOMAIN 119 122
FT POLY-ALA.
FT POLY-GLN.
FT DOMAIN 205 208
SQ SEQUENCE 368 AA; 40135 MW; 5CB75EB7E190BED4 CRC64;

Query Match 29.4%; Score 561.5; DB 1; Length 368;
Best Local Similarity 36.0%; Pred. No. 4,9e-29;
Matches 142; Conservative 70; Mismatches 127; Indels 55; Gaps 12;

OY 1 MLVYVTKLGFHEIRVQPNDTIMAVKKNIEIQQKDSYPMGQQLIFNGVKLDESTLE 60
DB 1 MNLTFKNIQQQKFVIVSDVADTKISELK--EKIQQNGNEVERKUKLIYSGRLADKTVG 58
OY 61 ENKVNEDGLVYMLSKGTSGSTGTSSQSHNTPATRQAPLEAPQAPQPVAPI--TT 118
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Db 59 EYKEDDFVCMVSRKSTSTPKSA--SPAPN--PAPVPEKVEPSTVVEST 112
Qy 119 SOPEGLPAQPNTHDNASN-----LLSGRNVDTIINLMGSGSWDKDYQALR 170
Db 113 STGTQTAAPNSNDTATSEAPIDANTLVAGNRNAVEMVMG--YRSEVERAMR 169
Qy 171 AAYNPERAVEYLSGIP-----VTAEIAPVIGGANTTDRAPTGAGLSIPNAPL 224
Db 170 AAFNPNRAVEYLTGIPEDILNRRESEAAALAAQOQSALAPTSTG-----QPA 221
Qy 225 DLPRQGA-----SNAGGAGGEPDLFLRNNPQFQAVREVNHPQILQPMVLKSN 277
Db 222 NLEQALSENENQPSNTVGDPLGLKSTIPQQLRQIVQGNPQMLTIIQIGOGD 281
Qy 278 POLRLTEHNDEFLQLINEPEFGEGEDFLDQPEDEMPHA---ISVYPERQALGRLES 334
Db 282 PALAQAOTNPENAFLOLL---AEGAG-----ESALPSGIGIQTQESSEIDRLCQ 331
Qy 335 MGEDRAVIEAFACDRNEELIANYLLEHAGEED 368
Db 332 LGFDRNIVIOAYLACDKNEELIANYLFEHGHSE 365

RESULT 6
RA23_YEAST STANDARD; PRT; 398 AA.
AC P32628;
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-1993 (Rel. 27, Last sequence update)
DE UV excision repair protein RAD23.
GN RAD23 OR YEL037C OR SYCP-ORF29.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94067136; Pubmed=8246991;
RA Watkins J.F., Sung P., Prakash L., Prakash S.;
RT "The Saccharomyces cerevisiae DNA repair gene RAD23 encodes a nuclear
RT protein containing a ubiquitin-like domain required for biological
RT function."
RL Mol. Cell. Biol. 13:7757-7765(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., Komp C.,
RA Wei Y., Taylor P., Nakahara K., Roberts D., Davis R.W.;
RT Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=S288C / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Hunnicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Hysanale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Patel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yellon M., Botstein D., Davis R.W.;
RT Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN=B-6441;
RA MEDLINE=94016558; Pubmed=841151;
RA Melnick L., Sherman F.;
RT "The gene clusters ARC and COR on chromosomes 5 and 10, respectively,
RT of Saccharomyces cerevisiae share a common ancestry."
RL J. Mol. Biol. 233:372-388(1993).
CC - SUBCELLULAR LOCATION: Nuclear (Probable).
CC - SIMILARITY: CONTAINS 1 UBIOUITIN-LIKE DOMAIN.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L25428; AAL16070.1; -
DR EMBL; U18779; AAB65005.1; -
DR EMBL; L22172; AAA34935.1; -
DR EMBL; L22173; AAA34938.1; -
DR EMBL; S65964; AAD13972.1; -
DR EMBL; S66117; AAB28441.1; -
DR PIR; S30845; S30845.
DR HSSP; P54725; IDVO.
DR SGD; S0000763; RAD23.
DR InterPro; IPR004806; Rad23.
DR InterPro; IPR000449; UBA_domain.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; Ubiquitin; 1.
DR Pfam; PF00627; UBA; 2.
DR SMART; SM00165; UBA; 2.
DR SMART; SM00213; UBO; 1.
DR TIGRfam; TIGR00601; rad23; 1.
DR PROSITE; PS50053; UBIOUITIN_2; 1.
DR DNA damage; DNA repair; Nuclear protein.
FW DOMAIN 1 77 UBIOUITIN-LIKE.
FT CONFLICT 277 77
SEQUENCE 398 AA; 42366 MW; B3F04360BAB60B833 CRC64;

Query Match 21.1%; Score 403; DB 1; Length 398;
Best Local Similarity 31.7%; Pred. No. 7e-19;
Matches 130; Conservative 63; Mismatches 157; Indels 60; Gaps 16;

Qy 1 MKLVKTLKGNHFRPQNDITMAVK-KNTEELQGDSTYWGQGLIFNGKVLKDESTL 59
Db 2 VSLTFKFKKKKVPUDLEPSNTLTETKTLAQSISCESS---QIKLISGKVLQDSKTV 57
Qy 60 EENKVNEDGLVVMISKGTSGSTGSSSHSNTPAFQAPPLPAPOA---POPPAPI 116
Db 58 SEGKIKGDQYVFNVSQK---STKTKVTEPPIAPESAITTPGGRNSTEASSTASAPRA 114
Qy 117 TT-----SOP-EGRLPAQPNTHDNASNLLSGRNVDTIINLMGSGSWDKDYQALRA 171
Db 115 ATAPEGSQPDEQATERTESASTPGFVGTERTETIERIMENG---YQREVERALRA 171
Qy 172 AAYNPERAVEYLSGIPPTAEIAPVIGGANTTDRAPTGAGLSGIPNAPLFLFQGA 231
Db 172 AFNPNRAVEYLTGIP--ENLRQPEPQOTAAAEOPSTATTAEOP--AEDDLFAQAA 227
Qy 232 --SNAGGA---GGCPDLFLRNNP-----QFOAVREVNHPQILQPMVLKSN 277
Db 228 OGGAASSGALGTGATDAAGCGPGSIGLVEDLISLRQVSSGNPEALALENISARY 287
Qy 278 POLRLTEHNDEFLQLINEP-----FEGG---EGDFLD-----OPEDEEM 315
Db 288 POLREHIANAEVYVSMLEAVGNMODVMGADDMVEGEDIETVGERAAAGLQGGREG 347
Qy 316 PHAIVSPEREQALGRLESMGFDRARVTEAFACDRNEELIANYLLEHAGEED 364
Db 348 SFQYDYLTPEDDAISRLCELEFERDLVLYQVFACDKNEELIANYLFEHGHSE 397

RESULT 7
YAUD_SCHPO STANDARD; PRT; 354 AA.
AC Q10163;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C26A3.16 in chromosome I.
GN SPAC26A3.16.
OS Schizosaccharomyces pombe (Fission yeast).
```

```

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21048401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne R., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., Mclean J.,
RA Moore P., Moule S., Mungall K., Murphy L., Niblett D., Oell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wandut R., Purrelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: TO YEAST DSK2.
CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.
CC -----
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CC -----
CC EMBL; 269240; CAA93239.1; -
CC InterPro: IPR000449; UBA_domain.
CC InterPro: IPR000626; Ubiqultin.
CC Pfam: PF00627; UBA; 1.
CC Pfam: PF00627; UBA; 1.
CC SMART; SM00165; UBA; 1.
CC SMART; SM00213; UBO; 1.
CC PROSITE; PS50053; UBIQUITIN_2; 1.
CC Hypothetical protein.
CC DOMAIN 1 78 UBIQUITIN-LIKE.
CC SEQUENCE 354 AA; 36819 MW; 1A99B2D97E73A831 CRC64;

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Query Match 8.6%; Score 163.5; DB 1; Length 354;
Best Local Similarity 22.7%; Pred. No. 0.0012;
Matches 95; Conservative 62; Mismatches 134; Indels 127; Gaps 21;

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OY 1 MLTYVTKLGTPEIRVQNDITMAVKNIIEIQGDSIFPGQQLIIFNGKYLKDESTLE 60
DB 4 ISLTIRKANDOKYAVTVDESSVLAKKAIVADIEK---ERORLIYAGRVLKDESESLK 60
OY 61 ENKVNEDGFLVYMLSKSGTSGTSSQHSNTPATROAPLEAPQQAQPPAPVPTTQ 120
DB 61 TKRIODGHSIHLYKTLIGQPPAAATVNSDR-----TQQVPTNIQAGQANNPLANTTSAR 115
OY 121 PEG---LPAQA-----PNTHDNAASNLISGRVVTIIN-----OLMEV----- 155
DB 116 YAGFNIPMSASAMFGPNPENPVPPSTEELA--NMLSNPVOSSINMFSNPMQLDMITNS 173

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OY 156 -----GGGMDKDKVOR-ALRAAYNNDP--RAVEYLY-----SGIPVTAIEAVPIGGQA 202
DB 174 SPLRLNAPPYVRQMQSPERRRAMTBDPTROMAQIHOQMGAGIDPMISMIGGLGAGI 233
OY 203 NNTDRAPPTGAGISGIPNTAPRLDLFPQASNAGCG--AGSGPLDPLFNNNPQFQAVRMVHT 261
DB 234 -----GLGGAGLGGR-----GGANNATAGTAGAPVD-----QTAAANTT--- 269
OY 262 NPQILQPMVLVSKNPQILRLIEHNHDEFQLNLE-----PEDEGECG-----F 306
DB 270 -----QN-----LLNNGGAGFGAGIGDAGLGAGCGAAS 299
OY 307 LDQPEDEMPHAISVPEEQ--EAIGLESMGF--DRARYTEAFACDRNEELANTLL 361
DB 300 PPAADPTRP-----PEERYADQLSOLNMGCFVDEFRVQALRRSGVNOGATIESLL 351

RESULT 8
DSK2_YEAST STANDARD; PRT; 373 AA.
ID DSK2_YEAST
AC P48510;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ubiqultin-like protein DSK2.
GN DSK2 OR SHE4 OR YMR276W OR YMR8021.02.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C;
RX MEDLINE=96281973; PubMed=8682868;
RA Biggins S., Ivanovska I., Rose M.D.;
RT "Yeast ubiquitin-like genes are involved in duplication of the
RT microtubule organizing center.";
RL J. Cell Biol. 133:1331-1346(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C / AB972;
RA Pearson D., Bowman S., Barrett B.G., Rajandream M.A.;
RL Submitted (Mar-1995) to the EMBL/GenBank/DBD databases.
CC -1- FUNCTION: INVOLVED, WITH RAD23 IN SPINDLE POLE BODY DUPLICATION.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: TO S.POMBE SPAC256A3.16.
CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.
CC -----
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CC -----
CC EMBL; L40587; AAB07267.1; -
CC EMBL; 249704; CAA89774.1; -
CC HSSP; 015843; INDD.
CC SGD; S0004889; DSK2.
CC InterPro: IPR000449; UBA_domain.
CC InterPro: IPR000626; Ubiqultin.
CC Pfam: PF00240; ubiqultin; 1.
CC Pfam: PF00627; UBA; 1.
CC SMART; SM00165; UBA; 1.
CC SMART; SM00213; UBO; 1.
CC PROSITE; PS00299; UBIQUITIN_1; 1.
CC PROSITE; PS50053; UBIQUITIN_2; 1.
CC Hypothetical protein.
CC DOMAIN 1 76 UBIQUITIN-LIKE.
CC FT CONFLICT 109 109 R -> A (IN REF. 2).
CC FT CONFLICT 296 296 R -> A (IN REF. 2).
CC SEQUENCE 373 AA; 39516 MW; 25EDF82B9DB67DF6 CRC64;

```


RA Guarino L.A.;
 RT "Identification of a viral gene encoding a ubiquitin-like protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:409-413(1990).
 RN [9]
 RP SEQUENCE FROM N.A.
 RC SPECIES-M.sexita;
 RA MEDLINE-91000673; PubMed-2169771;
 RX Schwartz L.M., Myer A., Kozs L., Engelstein M., Maller C.;
 RT "Activation of polyubiquitin gene expression during developmentally
 RT programmed cell death.";
 RL Neuron 5:411-419(1990).
 RN [10]
 RP SEQUENCE FROM N.A.
 RC SPECIES-M.sexita; TISSUE-Pupae;
 RX MEDLINE-91045065; PubMed-1700368;
 RA Bishop S.T., Schwartz L.M.;
 RT "Characterization of a ubiquitin-fusion gene from the tobacco
 RT hawmoch, Manduca sexta.";
 RL Nucleic Acids Res. 18:6039-6043(1990).
 CC -I- FUNCTION: Involved in the ATP-dependent selective degradation of
 CC cellular proteins, the maintenance of chromatin structure, the
 CC regulation of gene expression, the stress response, and ribosome
 CC biogenesis.
 CC -I- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -I- MISCELLANEOUS: Ubiquitin is synthesized as a polyubiquitin
 CC precursor with exact head to tail repeats, the number of repeats
 CC differs between species (up to 12 in Xenopus). In some species
 CC there is a final amino-acid after the last repeat. Some ubiquitin
 CC genes contain a single copy of Ubiquitin fused to a ribosomal
 CC protein (either L40 or S27A).
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 CC -----
 DR EMBL; M3013; AAA28999.1; -;
 DR EMBL; M3015; AAA29001.1; -;
 DR EMBL; M3312; AAA29007.1; -;
 DR EMBL; M2248; AAA28997.1; ALT_TERM.
 DR EMBL; M2256; AAA28998.1; ALT_TERM.
 DR EMBL; X53059; CAA37227.1; ALT_TERM.
 DR EMBL; X59943; CAA42568.1; ALT_TERM.
 DR EMBL; X69119; CAA48871.1; -;
 DR EMBL; AE003479; AAG22240.1; ALT_TERM.
 DR EMBL; AE003479; AAG22241.1; ALT_TERM.
 DR EMBL; AE003577; AAF51034.1; ALT_TERM.
 DR EMBL; AE003628; AAF52941.1; ALT_TERM.
 DR EMBL; M30306; AAA29989.1; ALT_SEQ.
 DR EMBL; X53524; CAA37599.1; ALT_TERM.
 DR PIR; A02575; UQPRM.
 DR PIR; B31560; UQPR7.
 DR PIR; B34813; UQURSF.
 DR PIR; S13136; UQW07A.
 DR PIR; A26087; A2607A.
 DR PIR; A31560; A31560.
 DR PIR; JH0302; JH0302.
 DR PIR; S10319; S10319.
 DR PIR; S23988; S23988.
 DR FlyBase; FBgn0003941; RPL40.
 DR FlyBase; FBgn0003942; RPS27A.
 DR FlyBase; FBgn0003943; UBI-PS3E.
 DR InterPro; IPR000626; ubiquitin.
 DR PROSITE; PS00299; UBIOUTFIN_1; 1.
 DR PROSITE; PS50053; UBIOUTFIN_2; 1.
 KM Nuclear protein; Polyprotein.
 FT SITE 48 48
 FT BINDING 54 54
 FT SITE 68 68
 FT ESSENTIAL FOR FUNCTION.

FT BINDING 72 72 CONJUGATION TO ACTIVATING ENZYME.
 FT BINDING 76 76 CONJUGATION TO ACCEPTOR PROTEINS.
 SQ SEQUENCE 76 AA; 8565 MW; CA2A35397EFD9B52 CRC64;
 Query Match 6.4%; Score 122.5; DB 1; Length 76;
 Best Local Similarity 40.5%; Pred. No. 0.065;
 Matches 30; Conservative 14; Mismatches 27; Indels 3; Gaps 1;
 QY 1 MKLTVTKTGTHREINRPNDTMAVKNEIEQKDSYPMGQOLLIFNGKVLKDESTLE 60
 DB 1 MQLFVTKITGKTTLEVEPSDTIENVK---AKIQDKEGIPPDQRLIFAGKQLDEDTLS 57
 QY 61 ENKNEDGELVYML 74
 DB 58 DYNQKESTLHVL 71
 RESULT 10
 ID UBIQ_HUMAN STANDARD; PRT; 76 AA.
 AC P02248; P02249; P02250; Q29120; Q91887; Q91888;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-ANG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ubiquitin.
 GN (UBA52 OR UBCEP2) AND UBB AND UBC AND (UBA80 OR UBCEP1 OR RPS27A).
 OS Homo sapiens (Human).
 OS Mus musculus (Mouse).
 OS Rattus norvegicus (Rat).
 OS Bos taurus (Bovine).
 OS Cavia porcellus (Guinea pig).
 OS Cricetus griseus (Chinese hamster).
 OS Oryctolagus longicaudatus (Long-tailed hamster) (Chinese hamster).
 OS Sus scrofa (Pig).
 OS Gallus gallus (Chicken), and
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606, 10090, 10116, 9913, 10141, 10029, 10030, 9986, 9823,
 OX 9031, 8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Human;
 RX MEDLINE-85230546; PubMed-2988935;
 RA Wborg O., Pedersen M.S., Wind A., Berglund L.E., Marcker K.A.,
 RA Vuust J.;
 RT "The human ubiquitin multigene family: some genes contain multiple
 RT directly repeated ubiquitin coding sequences.";
 RL EMBO J. 4:755-759(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Human;
 RX MEDLINE-87326412; PubMed-2820408;
 RA Einspander R., Sharma H.S., Schelt K.H.;
 RT "Cloning and sequence analysis of a cDNA encoding poly-ubiquitin in
 RT human ovarian granulosa cells.";
 RL Biochem. Biophys. Res. Commun. 147:581-587(1987).
 RN [3]
 RP SEQUENCE FROM N.A. (UBB).
 RC SPECIES-Human; TISSUE-Lymphocytes;
 RX MEDLINE-87146371; PubMed-3029682;
 RA Baker R.T., Board P.G.;
 RT "The human ubiquitin gene family: structure of a gene and pseudogenes
 RT from the UB B subfamily.";
 RL Nucleic Acids Res. 15:443-463(1987).
 RN [4]
 RP SEQUENCE FROM N.A. (UBA52).
 RC SPECIES-Human;
 RX MEDLINE-912181; PubMed-1850507;
 RA Baker R.T., Board P.G.;
 RT "The human ubiquitin-52 amino acid fusion protein gene shares several
 RT structural features with mammalian ribosomal protein genes.";

RL Nucleic Acids Res. 19:1035-1040(1991).
RN
RN [5]
RC SEQUENCE OF 5-76 FROM N.A. (UBA80).
RC SPECIES-Human;
RX MEDLINE-85207809; PubMed-2581967;
RA Lund P.K., Moats-Staats B.M., Simmons J.G., Hoyt E., D'Ercole A.J.,
RA Martin F., van Wyk J.J.;
RT "Nucleotide sequence analysis of a cDNA encoding human ubiquitin
RT reveals that ubiquitin is synthesized as a precursor.";
RL J. Biol. Chem. 260:7609-7613(1985).
RN
RN [6]
RC SEQUENCE OF 1-74.
RC SPECIES-Human;
RX MEDLINE-75156547; PubMed-124018;
RX Schlesinger D.H., Goldstein G.;
RT "Hybrid tropomyosin reconstituted from vertebrate and arthropod
RT subunits.";
RL Nature 255:423-424(1975).
RN
RN [7]
RC SEQUENCE FROM N.A.
RC SPECIES-Mouse; STRAIN-C57BL/6;
RX MEDLINE-90245601; PubMed-2159627;
RA Finch J.S., Bonham K., Kriegl P., Bowden G.T.;
RT "Murine polyubiquitin mRNA sequence.";
RL Nucleic Acids Res. 18:1907-1907(1990).
RN
RN [8]
RC SEQUENCE.
RC SPECIES-Rat; STRAIN-Wistar; TISSUE-Duodenum;
RX MEDLINE-94304928; PubMed-8031840;
RA Hubbard M.J., Carne A.;
RT "Differential feeding-related regulation of ubiquitin and
RT calbindin9kda in rat duodenum.";
RL Biochim. Biophys. Acta 1200:191-196(1994).
RN
RN [9]
RC SEQUENCE FROM N.A. (UBA52).
RC SPECIES-Rat; STRAIN-Sprague-Dawley;
RX MEDLINE-96011832; PubMed-7488009;
RA Chan Y.-L., Suzuki K., Wool I.G.;
RT "The carboxyl extensions of two rat ubiquitin fusion proteins are
RT ribosomal proteins s27a and l40.";
RL Biochem. Biophys. Res. Commun. 215:682-690(1995).
RN
RN [10]
RC SEQUENCE FROM N.A.
RC SPECIES-Bovine; TISSUE-Seminal vesicle;
RX MEDLINE-93176814; PubMed-8382528;
RA Wempe F., Scheit K.H.;
RT "Characterization of a full-length cDNA encoding a bovine four
RT tandem-repeat ubiquitin.";
RL Biochim. Biophys. Acta 1172:209-211(1993).
RN
RN [11]
RC SEQUENCE OF 1-74.
RC SPECIES-Bovine;
RX MEDLINE-75205496; PubMed-1170880;
RA Schlesinger D.H., Goldstein G., Miall H.D.;
RT "The complete amino acid sequence of ubiquitin, an adenylate cyclase
RT stimulating polypeptide probably universal in living cells.";
RL Biochemistry 14:2214-2218(1975).
RN
RN [12]
RC SEQUENCE OF 1-50.
RC SPECIES-Bovine;
RX MEDLINE-81062406; PubMed-6254502;
RA Hamilton J.W., Rouse J.B.;
RT "The biosynthesis of ubiquitin by parathyroid gland.";
RL Biochem. Biophys. Res. Commun. 96:114-120(1980).
RN
RN [13]
RC SEQUENCE FROM N.A.
RC SPECIES-Pig;
RX MEDLINE-88054463; PubMed-2824145;
RA Einspanier R., Sharma H.S., Scheit K.H.;
RT "An mRNA encoding poly-ubiquitin in porcine corpus luteum:
RT identification by cDNA cloning and sequencing.";
RL DNA 6:395-400(1987).
RN
RN [14]

RP SEQUENCE FROM N.A.
RC SPECIES-C.porcillus; TISSUE-Spleen;
RA Tsukagoshi N.;
RT "Ascorbate-dependent expression of ubiquitin genes in guinea pig.";
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN
RN [15]
RC SEQUENCE FROM N.A.
RC SPECIES-C.griseus; STRAIN-V79; TISSUE-Lung fibroblast;
RX MEDLINE-92223105; PubMed-1314094;
RA Nenoi M., Mita K., Ichimura S.;
RT "Evolutionarily conserved structure of the 3' non-translated region
RT of a Chinese hamster polyubiquitin gene";
RL Biochim. Biophys. Acta 1150:247-252(1992).
RN
RN [16]
RC SEQUENCE FROM N.A.
RC SPECIES-C.longicaudatus; STRAIN-V79; TISSUE-Lung fibroblast;
RX MEDLINE-89160248; PubMed-2537950;
RA Fornace A.J. Jr., Alamo I. Jr., Hollander M.C., Lamoreaux E.;
RT "Ubiquitin mRNA is a major stress-induced transcript in mammalian
RT cells.";
RL Nucleic Acids Res. 17:1215-1230(1989).
RN
RN [17]
RC SEQUENCE.
RC SPECIES-Rabbit; TISSUE-Brain;
RX MEDLINE-93149997; PubMed-1337207;
RA Wajih N., Siddiqi A.R., Kaiser R., Persson B., Zaidi Z.H.,
RT Joernvall H.;
RT "Structural characterization of rabbit brain ubiquitin.";
RL Protein Seq. Data Anal. 5:31-32(1992).
RN
RN [18]
RC SEQUENCE FROM N.A.
RC SPECIES-Chicken;
RX MEDLINE-85213498; PubMed-2987683;
RA Bond U., Schlesinger M.J.;
RT "Ubiquitin is a heat shock protein in chicken embryo fibroblasts.";
RL Mol. Cell. Biol. 5:949-956(1985).
RN
RN [19]
RC SEQUENCE FROM N.A.
RC SPECIES-Chicken;
RX MEDLINE-87089821; PubMed-3025663;
RA Bond U., Schlesinger M.J.;
RT "The chicken ubiquitin gene contains a heat shock promoter and
RT expresses an unstable mRNA in heat-shocked cells.";
RL Mol. Cell. Biol. 6:4602-4610(1986).
RN
RN [20]
RC SEQUENCE FROM N.A.
RC SPECIES-Chicken; TISSUE-Spermatid;
RX MEDLINE-8908351; PubMed-2850543;
RA Mezquita J., Pau M., Mezquita C.;
RT "cDNA encoding a chicken ubiquitin-fusion protein identical to the
RT corresponding human protein.";
RL Nucleic Acids Res. 16:11838-11838(1988).
RN
RN [21]
RC SEQUENCE FROM N.A.
RC SPECIES-X.laevis;
RX MEDLINE-85048942; PubMed-6209017;
RA Dworkin-Rasli E., Shrutkowski A., Dworkin M.B.;
RT "Multiple ubiquitin mRNAs during Xenopus laevis development contain
RT tandem repeats of the 76 amino acid coding sequence.";
RL Cell 39:321-325(1984).
RN
RN [22]
RC X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RC SPECIES-Human;
RX MEDLINE-87311725; PubMed-3041007;
RA Vijay-Kumar S., Bugg C.E., Cook W.J.;
RT "Structure of ubiquitin refined at 1.8-A resolution.";
RL J. Mol. Biol. 194:531-544(1987).
RN
RN [23]
RC X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RC SPECIES-Human;
RX MEDLINE-94220022; PubMed-8166633;
RA Ramage R., Green J., Muir T.W., Ogunjobi O.M., Love S., Shaw K.;
RT "Synthetic, structural and biological studies of the ubiquitin system:

Query Match 6.4%; Score 122.5; DB 1; Length 76;
Best Local Similarity 40.5%; Pred. No. 0.065;
Matches 30; Conservative 14; Mismatches 27; Indels 3; Gaps 1;

1 MKLVYTLGTPEIRHVONNDITMAVKNNIEEIKGDSYPMWGOQLIFNGKYLKDSSTLE 60
1 MOLFVKTLTGKTTTLEVEVDITENYK---AKIQKEGIPPDQRLIFAGKOLEDERTLS 57

61 ENKVEDGFVYVNL 74
58 DYNIOKESTLHLVL 71

RESULT 11
ID RFX1_HUMAN STANDARD; PRT; 979 AA.
AC P22670;
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE MHC class II regulatory factor RFX1 (RFX) (Enhancer factor C) (EF-C).
GN RFX1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91071581; PubMed=2253877;
RA Reith W., Sanchez-Herrero C., Kober M., Silacci P., Bette C.,
RA Barras E., Mach B.;
RT "MHC class II regulatory factor RFX has a novel DNA-binding domain
and a functionally independent dimerization domain.";
RL Genes Dev. 4:1528-1540(1990).
RN [2]
RP IDENTITY BETWEEN RFX1 AND EF-C.
RX MEDLINE=94019311; PubMed=8413236;
RA Siegrist C.A., Durand B., Emery P., David E., Hearing P., Mach B.,
RA Reith W.;
RT "RFX1 is identical to enhancer factor C and functions as a
transactivator of the hepatitis B virus enhancer.";
RL Mol. Cell. Biol. 13:6375-6384(1993).
RN [3]
RP BINDING TO RPL30 PROMOTER.
RX MEDLINE=94040774; PubMed=8224874;
RA Saitany G., Perry R.P.;
RT "Transcription factor RFX1 helps control the promoter of the mouse
ribosomal protein-encoding gene rpl30 by binding to its alpha
element.";
RL Gene 132:279-283(1993).
RN [4]
RP SHOWS THAT BLS IS NOT DUE TO RFX1.
RX MEDLINE=92375076; PubMed=1508204;
RA Sanchez-Herrero C., Reith W., Silacci P., Mach B.;
RT "The DNA-binding defect observed in major histocompatibility complex
class II regulatory mutants concerns only one member of a family of
Mol. Cell. Biol. 12:4076-4083(1992).
RN [5]
RP FUNCTION: REGULATORY FACTOR ESSENTIAL FOR MHC CLASS II GENE
EXPRESSION. BINDS TO THE X BOXES OF MHC CLASS II GENES. ALSO BINDS
TO AN INVERTED REPEAT (ENH) REQUIRED FOR HEPATITIS B VIRUS GENES
EXPRESSION AND TO THE MOST UPSTREAM ELEMENT (ALPHA) OF THE RPL30
PROMOTER.
CC -1- SUBUNIT: BINDS DNA AS AN HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE RFX FAMILY.

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DR EMBL: X58964; CAA41730.1; -
DR EMBL: A20498; CAA01506.1; -
DR PIR: A35913; A35913.
DR TRANSFAC: T00909; -
DR TRANSFAC: T01673; -
DR GeneW: HGNC:9982; RFX1.
DR MIM: 600006; -
DR InterPro: IPR003150; RFX_DNA_binding.
DR Pfam: PF02257; RFX_DNA_binding; 1.
KW DNA-binding; Transcription regulation; Activator; Nuclear protein.
FT DOMAIN 381 411 GLY-RICH.
FT DNA_BIND 438 528 EXPERIMENTALLY DEDUCED.
FT DOMAIN 920 936 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 744 979 NECESSARY FOR DIMERIZATION.
SQ SEQUENCE 979 AA; 104728 MW; 556151F86C6AC9A2 CRC64;

Query Match 6.4%; Score 122; DB 1; Length 979;
Best Local Similarity 25.8%; Pred. No. 1.9;
Matches 48; Conservative 31; Mismatches 75; Indels 32; Gaps 10;

75 SKGKTSGS--TGTSSSQ-----HSNTPARQAPLEAPQAPQP--PVAFITTS--QPEGL 124
216 SSSKTAGAPRTGVPQQLQYGVQOVSVPYQERSVQATQAPKPGVQPLTVQGLQPVHV 275
125 PAQAPRTHDMAASNLGSGNVDTIINQLMEMGSGSDKDKVORALRAA--YNNPE----- 177
276 AGEVQOQLQVPPVPHYS-----SQVQYVEG--DASTYSATISSYSPPEPLTYQ 325
178 RAVEYLSCIPYTAETAVDIPGCGANTTDRAPTGAGLSGIPNTPALDLPFGASNA--G 235
326 TASTSYEAAGTATQVTPATSQAVASGSMPIWYSGQVVASASTG--AGASNSGCG 382
236 GGAGCG 241
383 GSGGGG 388

RESULT 12
ID NED8_HUMAN STANDARD; PRT; 81 AA.
AC Q15843;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ubiquitin-like protein NED8.
GN NED8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TTSUB-Fibrosarcoma;
RX MEDLINE=98361870; PubMed=9694792;
RA Osaka F., Kawasaki H., Aida N., Saeki M., Chiba T., Kawashima S.,
RA Tanaka K., Kato S.;
RT "A new NED8-ligating system for cullin-4A.";
RL Genes Dev. 12:2263-2268(1998).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RX MEDLINE=99074275; PubMed=9857030;
RA Whibby F.G., Xia G., Pickart C.M., Hill C.P.;
RT "Crystal structure of the human ubiquitin-like protein NED8 and
interactions with ubiquitin pathway enzymes.";
RN [3]
RP FUNCTION: ACTIVATED BY AN E1-LIKE COMPLEX, CONSISTING OF APP-B1
AND UBA3 AND THEN LINKED TO THE E2-LIKE ENZYME, UBC12. THE MAJOR
TARGET PROTEIN MODIFIED BY NED8 IS CULLIN-4A.
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE DURING THE EMBRYONIC
CC DEVELOPMENT AND DIFFERENTIATION OF THE CENTRAL NERVOUS SYSTEM. MAY

FT BINDING 76 76 CONJUGATION TO ACCEPTOR PROTEINS.
SQ SEQUENCE 76 AA: 8551 MW: C59A35397ERC9B53 CRC64;

Query Match 6.3%; Score 120.5; DB 1; Length 76;
Best Local Similarity 40.5%; Pred. No. 0.088;
Matches 30; Conservative 14; Mismatches 27; Indels 3; Gaps 1;

OY 1 MKLTVKTLKGTHFEIRVQNDITIMAVKKNIEIQQKDSYPMGQQLIFNGKYLKDESTLE 60
DB 1 MQLFVKTLTGKTIITLDPERSDIENVK--AKIQDEKGIIPDQRLIFAGKQLEDGRTLS 57
OY 61 ENKVNEDGFLVYML 74
DB 58 DYNIOKESTLHLVL 71

RESULT 15

ID UBIO_LEIMA STANDARD; PRT; 76 AA.
AC Q05550; 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Ubiquitin.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MHOM/IR/83/LT252;
RX MEDLINE=93380668; PubMed=8396548;
RA Graeff G.R., Steele P.M., Peterson C.L., Bennett M.L., Langer P.J.;
RT "Sequence of a Leishmania major gene encoding an ubiquitin fusion
protein.";
RL Gene 131:155-156(1993).
CC -! FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF
CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE
REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
BIogenesis.
CC -! SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -! MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED WITH RIBOSOMAL CEP52 AS
ITS C-TERMINAL EXTENSION.
CC -----
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DR EMBL; 214232; CAA78598.1; -.
DR HSSP; P02248; IUBI.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin, 1.
DR PRINTS; PR00348; UBQUITIN.
DR SMART; SM00213; UBQ; 1.
DR PROSITE; PS00299; UBQUITIN_1; 1.
DR PROSITE; PS50053; UBQUITIN_2; 1.
KW Nuclear protein; Polypeptide
FT SITE 48
FT BINDING 76
FT SEQUENCE 76 AA: 8549 MW: C52648497FFD8E47 CRC64;
SQ

Query Match 6.2%; Score 118.5; DB 1; Length 76;
Best Local Similarity 39.2%; Pred. No. 0.12; Mismatches 27; Indels 3; Gaps 1;

OY 1 MKLTVKTLKGTHFEIRVQNDITIMAVKKNIEIQQKDSYPMGQQLIFNGKYLKDESTLE 60
DB 1 MQLFVKTLTGKTIITLDPERSDIENVK--AKIQDEKGIIPDQRLIFAGKQLEDGRTLS 57

OY 61 ENKVNEDGFLVYML 74
DB 58 DYNIOKESTLHLVL 71
Search completed: November 4, 2002, 02:00:37
Job time : 15.806 secs